

2651224_1.TXT
SEQUENCE LISTINGS

<110> INJE UNIVERSITY
 <120> CANCER CELL TARGETING GENE DELIVERY METHOD
 <130> Q94769
 <140> US 10/578,839
 <141> 2006-05-10
 <150> KR 10-2003-0079897
 <151> 2003-11-12
 <150> PCT/KR2004/000545
 <151> 2004-03-15
 <160> 11
 <170> KopatentIn 1.71
 <210> 1
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Env F primer
 <400> 1
 cgcggatccg aattccatac ctggtgttgc tgacta 36
 <210> 2
 <211> 47
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> 597LN primer
 <400> 2
 agctggacct ggctgccacc acctccgcta ttttggtccc attttac 47
 <210> 3
 <211> 49
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> LC597 primer
 <400> 3
 caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa 49
 <210> 4
 <211> 35
 <212> DNA

<213> Artificial Sequence

<220>

<223> Spike R2 primer

<400> 4

tgctctagaa ttcttaaagg ttaccttcgt tctct

35

<210> 5

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> LnkNScFv primer

<400> 5

ggaggtggtg gcagccaggt ccagctagtg cagtct

36

<210> 6

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> ScFvLnkC primer

<400> 6

actgcctcct ccacctgcgg cggggttgaa gtccca

36

<210> 7

<211> 2058

<212> DNA

<213> Gibbon Ape leukemia virus

<220>

<221> sig_peptide

<222> (1)..(126)

<220>

<221> misc_feature

<222> (127)..(1467)

<223> surface subunit region

<220>

<221> misc_feature

<222> (1468)..(2025)

<223> transmembrain domain

<400> 7

atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60

atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgcgtatt cggcggcggc 120

gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggctactg 180

2651224_1.TXT

tcccaaactg	gagacgttgt	ctgggataca	aaggcagtcc	agcccccttg	gacttggtgg	240
cccacactta	aacctgatgt	atgtgccttg	gcggctagtc	ttgagtcctg	ggatatccccg	300
ggaaccgatg	tctcgtcctc	taaacgagtc	agacctccgg	actcagacta	tactgccgct	360
tataagcaaa	tcacctgggg	agccataggg	tgcagctacc	ctcgggctag	gactagaatg	420
gcaagctcta	cctttctacgt	atgtccccgg	gatggccgga	ccctttcaga	agctagaagg	480
tgcggggggc	tagaatccct	atactgtaaa	gaatgggatt	gtgagaccac	ggggaccggt	540
tattggctat	ctaaatcctc	aaaagacctc	ataactgtaa	aatgggacca	aaatagcgaa	600
tggactcaaa	aatttcaaca	gtgtcaccag	accggctggg	gtaaccccct	taaaatagat	660
ttcacagaca	aaggaaaatt	atccaaggac	tggataacgg	gaaaaacctg	gggattaaga	720
ttctatgtgt	ctggacatcc	aggcgtacag	ttcaccattc	gcttaaaaat	caccaacatg	780
ccagctgtgg	cagtaggtcc	tgacctcgtc	cttgtggaac	aaggacctcc	tagaacgtcc	840
ctcgtctctc	cacctctctt	tcccccaagg	gaagcgccac	cgccatctct	ccccgactct	900
aactccacag	ccttggcgac	tagtgcacaa	actcccacgg	tgagaaaaac	aattgttacc	960
ctaaacactc	cgctctccac	cacaggcgac	agactttttg	atcttgtgca	gggggccttc	1020
ctaaccttaa	atgctaccaa	cccagggggc	actgagtctt	gctggctttg	tttggccatg	1080
ggccccctt	attatgaagc	aatagcctca	tcaggagagg	tcgcctactc	caccgacctt	1140
gaccggtgcc	gctggggggac	ccaaggaaag	ctcacctca	ctgagggtctc	aggacacggg	1200
ttgtgcatag	gaaaggtgcc	ctttacccat	cagcatctct	gcaatcagac	cctatccatc	1260
aattcctccg	gagaccatca	gtatctgctc	ccctccaacc	atagctggtg	ggcttgcagc	1320
actggcctca	ccccttgctt	ctccacctca	gtttttaatc	agactagaga	tttctgtatc	1380
cagggtccagc	tgattcctcg	catctattac	tatcctgaag	aagttttgtt	acaggcctat	1440
gacaattctc	accccaggac	taaaagagag	gctgtctcac	ttaccctagc	tgttttactg	1500
gggttgggaa	tcacggcggg	aataggtact	ggttcaactg	ccttaattaa	aggacctata	1560
gacctccagc	aaggcctgac	aagcctccag	atcgccatag	atgctgacct	ccggggccctc	1620
caagactcag	tcagcaagtt	agaggactca	ctgacttccc	tgtccgaggt	agtgtccaa	1680
aataggagag	gccttgactt	gctgtttcta	aaagaagggtg	gcctctgtgc	ggccctaaag	1740
gaagagtgtc	gtttttacat	agaccactca	ggtgcagtac	gggactccat	gaaaaaactc	1800
aaagaaaaac	tggataaaag	acagttagag	cgccagaaaa	gccaaaactg	gtatgaagga	1860
tggttcaata	actccccttg	gttcactacc	ctgctatcaa	ccatcgctgg	gccctatta	1920
ctcctccttc	tgttgctcat	cctcggggcca	tgcacatca	ataagttagt	tcaattcatc	1980
aatgatagga	taagtgcagt	taaaattctg	gtccttagac	aaaaatatca	ggccctagag	2040

aacgaaggta acctttaa

<210> 8
 <211> 786
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single-chain antibody Tag-72pS1 specific for Tag-72 surface antigen

<220>
 <221> misc_feature
 <222> (1)..(345)
 <223> heavy chain (H) variable region

<220>
 <221> misc_feature
 <222> (346)..(390)
 <223> (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (391)..(738)
 <223> light chain (L) variable region

<220>
 <221> misc_feature
 <222> (739)..(777)
 <223> PreS1 Tag

<220>
 <221> misc_feature
 <222> (778)..(786)
 <223> C-terminal extra termination sequence

<400> 8
 caggtccagc tagtgcagtc tggggctgaa gtgaagaagc ctggggccttc agtgaagggtg 60
 tcctgcaagg cttctggcta caccttcact gaccatgcaa ttactgggt gcgccaggcc 120
 cctggacaac gccttgagtg gatgggatat ttttctcctg gcaacgatga ttttaaatac 180
 tcccagaagt tccagggacg cgtgacaatc actgcagaca aatccgcgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac acggcggctt attactgtgc aagatcgttg 300
 aacatggcat actggggcca agggactctg gtcactgtct cttcagggtg aggcggttca 360
 ggcggagggtg gctctggcgg tggcggatcg gacattgtga tgaccagtc tccagactcc 420
 ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gagtgtttta 480
 tacagcagca acaataagaa ctacttagct tggtaccagc agaaaccagg acagcctcct 540
 aagctgctca ttactgggc atctaccgga gaatccgggg tccctgaccg attcagtggc 600
 agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660

2651224_1.TXT

gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaagggtg 720
 gaaatcaaag cggccgcagg agccaacgca aacaatccag attgggactt caacccccgcc 780
 gcatag 786

<210> 9
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PreS1 epitope

<400> 9
 Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro
 1 5 10

<210> 10
 <211> 2871
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ScFv-GaLV Env GP chimeric peptide (FVGEL199) DNA

<400> 10
 atggtattgc tgcctgggtc catgcttctc acctcaaacc tgcaccacct tcggcaccag 60
 atgagtcctg ggagctggaa aagactgatc atcctcttaa gctgctgatt cggcggcggc 120
 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggctactg 180
 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
 cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccc 300
 ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360
 tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg 420
 gcaagctcta ctttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480
 tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
 tattggctat ctaaatectc aaaagacctc ataactgtaa aatgggacca aaatagcgga 600
 ggtggtggca gccagggtcca gctagtgcag tctggggctg aagtgaagaa gcctggggct 660
 tcagtgaagg tgtcctgcaa ggcttctggc tacaccttca ctgacctatg aattcactgg 720
 gtgcgccagg cccctggaca acgccttgag tggatgggat atttttctcc tggcaacgat 780
 gattttaaat actcccagaa gttccaggga cgcgtgacaa tctactgcaga caaatccgag 840
 agcacagcct acatggagct gagcagcctg agatctgagg acacggcggt ctattactgt 900
 gcaagatcgt tgaacatggc atactggggc caagggactc tggtcactgt ctcttcaggt 960

2651224_1.TXT

ggaggcggtt caggcggagg tggctctggc ggtggcggt cggacattgt gatgacccag 1020
 tctccagact ccctggctgt gtctctgggc gagagggcca ccatcaactg caagtccagc 1080
 cagagtgttt tatacagcag caacaataag aactacttag cttggtacca gcagaaacca 1140
 ggacagcctc ctaagctgct catttactgg gcatctaccc gggaatccgg ggtccctgac 1200
 cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag cctgcaggct 1260
 gaagatgtgg cagtttatta ctgtcagcaa tattattcct atccgttgac gttcggccaa 1320
 gggaccaagg tggaaatcaa agcggccgca ggagccaacg caaacaatcc agattgggac 1380
 ttcaaccccg ccgcagggtg aggaggcagt gaatggactc aaaaatttca acagtgtcac 1440
 cagaccggct ggtgtaaccc ccttaaaata gatttcacag acaaaggaaa attatccaag 1500
 gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta 1560
 cagttcacca ttcgcttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc 1620
 gtccttgtgg aacaaggacc tcctagaacg tccctcgctc tcccacctcc tcttccccca 1680
 agggaagcgc caccgccatc tctccccgac tctaactcca cagccctggc gactagtgca 1740
 caaactccca cggtgagaaa aacaattgtt accctaaaca ctccgcctcc caccacaggc 1800
 gacagacttt ttgatcttgt gcagggggcc ttcctaacct taaatgctac caaccaggg 1860
 gccactgagt cttgctggct ttgtttggcc atgggcccc cttattatga agcaatagcc 1920
 tcatcaggag aggtcgctta ctccaccgac cttgaccggt gccgctgggg gaccaagga 1980
 aagctcacc cactgagggt ctcaggacac gggttgtgca taggaaagg gccccttacc 2040
 catcagcatc tctgcaatca gaccctatcc atcaattcct ccggagacca tcagtatctg 2100
 ctcccccca accatagctg gtgggcttgc agcactggcc tcacccttg cctctccacc 2160
 tcagttttta atcagactag agatttctgt atccaggctc agctgattcc tcgcatctat 2220
 tactatcctg aagaagtttt gttacaggcc tatgacaatt ctcaccccag gactaaaaga 2280
 gaggtgtct cacttaccct agctgtttta ctgggggttg gaatcacggc gggaatagg 2340
 actggttcaa ctgccttaat taaaggacct atagacctc agcaaggcct gacaagcctc 2400
 cagatcgcca tagatgctga cctccggggc ctccaagact cagtcagcaa gttagaggac 2460
 tcaactgactt ccctgtccga ggtagtgtc caaaatagga gaggccttga cttgctgttt 2520
 ctaaaagaag gtggcctctg tgccggcccta aaggaagagt gctgttttta catagaccac 2580
 tcaggtgcag tacgggactc catgaaaaaa ctcaaagaaa aactggataa aagacagtta 2640
 gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttact 2700
 accctgctat caaccatcgc tggggcccta ttactcctcc ttctgttgct catcctcggg 2760
 ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
 ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871

2651224_1.TXT

<210> 11
 <211> 956
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SCFV-GaLV Env GP chimeric ligand (FvGEL199)

<400> 11
 Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
 1 5 10 15
 Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
 20 25 30
 Leu Ser Cys Val Phe Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
 35 40 45
 Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
 50 55 60
 Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
 65 70 75 80
 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
 85 90 95
 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
 100 105 110
 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
 115 120 125
 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
 130 135 140
 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
 145 150 155 160
 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
 165 170 175
 Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
 180 185 190
 Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
 195 200 205
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 210 215 220
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
 225 230 235 240
 Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
 245 250 255
 Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
 260 265 270

2651224_1.TXT

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
 275 280 285
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
 290 295 300
 Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 305 310 315 320
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile
 325 330 335
 Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
 340 345 350
 Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
 355 360 365
 Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 370 375 380
 Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
 385 390 395 400
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 405 410 415
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
 420 425 430
 Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala
 435 440 445
 Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala
 450 455 460
 Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His
 465 470 475 480
 Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly
 485 490 495
 Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe
 500 505 510
 Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile
 515 520 525
 Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu
 530 535 540
 Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro
 545 550 555 560
 Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu
 565 570 575
 Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu
 580 585 590
 Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln
 595 600 605

2651224_1.TXT

Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser
 610 615 620
 Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala
 625 630 635 640
 Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
 645 650 655
 Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
 660 665 670
 Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
 675 680 685
 Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
 690 695 700
 His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
 705 710 715 720
 Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
 725 730 735
 Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
 740 745 750
 Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
 755 760 765
 Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
 770 775 780
 Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
 785 790 795 800
 Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
 805 810 815
 Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
 820 825 830
 Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
 835 840 845
 Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
 850 855 860
 Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
 865 870 875 880
 Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
 885 890 895
 Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
 900 905 910
 Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
 915 920 925
 Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
 930 935 940

2651224_1.TXT

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
945 950 955